





ATGGAACAGACGCTATTGATGGCTATATAACATGTGACAATGAGCTTTCACCCGAAGGGGAACACGCCA  
 TACCTTTGTCTGCGATAACTACCGATATATTGTACACTGTTACTCGAAAGTGGGCTTCCCCTTGTGCGGT 70  
 M E T D A I D G Y I T C D N E L S P E G E H A  
 ATATGGCCATTGACCTCACCTCAAGCAGGCCCAATGGACAGCAGCCTCGCCAAGTCACATGACAAGCAC 140  
 TATACCGGTAACCTGGAGTGGAGTTCGTGCGGGTTACCTGTCGTGCGGAGCGGTTCAAGTGTACTGTTCTGTG  
 N M A I D L T S S T P N G Q H A S P S H M T S T  
 AAATTCTGTAAAGCTGGAAATGCAGAGTGATGAAGAGTGTGACAGGCAGCCCCCTGAGCCGTGAGGATGAG 210  
 TTTAAGACATTTGACCTTTACGTCTCACTACTTCTCACACTGTCCGTGCGGGACTCGGCACTCCTACTC  
 N S V K L E M Q S D E E C D R Q P L S R E D E  
 ATCAGGGGCCACGATGAGGGGAGCAGCCTAGAAGAACCCTAATTGAGAGCAGCGAGGTGGCCGACAACA 280  
 TAGTCCCCGGTGCTACTCCCTCGTGGATCTTCTTGGGGATTAAGTCTCGTCCGCTCCACCGGCTGTTGT  
 I R G H D E G S S L E E P L I E S S E V A D N  
 GGAAAGTCCAGGACCTTCAAGGCGAGGGAGGAATCCGGCTTCCGAATGGTAAACTGAAATGTGACGTCTG 350  
 CCTTTCAGGTCTGGAAGTTCGGCTCCCTCCTTAGGCCGAAGGCTTACCATTGACTTTACACTGCAGAC  
 R K V Q D L Q G E G G I R L P N G K L K C D V C  
 TGGCATGGTTTGCATTGGGCCCAATGTGCTTATGGTACATAAAAGGAGTCACACTGGTGAGCGGCCCTTC 420  
 ACCGTACCAAACGTAACCCGGGTTACACGAATACCATGTATTTTCTCAGTGTGACCACTCGCCGGGAAG  
 G M V C I G P N V L M V H K R S H T G E R P F  
 CACTGTAACCAAGTCCGGAGCTTCTTTTACCCAGAAGGGCAACCTTCTGAGACAGATAAAGTTACACTCTG 490  
 GTGACATTGGTCACGCCTCGAAGAAAATGGGTCTTCCCGTTGGAAGACTCTGTGTATTTCAATGTGAGAC  
 H C N Q C G A S F T Q K G N L L R H I K L H S  
 GAGAGAAGCCCTTCAAATGTCTTTCTGTAGCTATGCTTGTAGAAGAAGGGACGCTCTCACAGGACACCT 560  
 CTCTCTTCGGGAAGTTTACAGGAAAGACATCGATACGAACATCTTCTCCCTGCGAGAGTGCTCTGTGGA  
 G E K P F K C P F C S Y A C R R R D A L T G H L  
 CAGGACCCATTCTGTGGGTAAACCTCACAAGTGTAACTACTGTGGCCGAAGCTACAAGCAGCGCACGTCA 630  
 GTCCTGGGTAAGACACCCATTTGGAGTGTTCACATTGATGACACCGGCTTCGATGTTCTGTCGCGTGCAGT  
 R T H S V G K P H K C N Y C G R S Y K Q R T S

FIG. 3  
(1 of 3)

CTGGAGGAACACAAGGAACGCTGTCACAACTATCTCCAGAATGTCAGCATGGAGGCTGCCGGGCAGGTCA 700  
GACCTCCTTGTTCTTGGGACAGTGTTGATAGAGGTCTTACAGTCGTACCTCCGACGGCCCGTCCAGT  
L E E H K E R C H N Y L Q N V S M E A A G Q V  
TGAGTCACCATGTAACGCTATGGAAGATTGTAAGGAACAAGAGCCTATCATGGACAACAATATTTCTCT 770  
ACTCAGTGGTACATGGCGGATACCTTCTAACATTCTTGTCTCGGATAGTACCTGTTGTTATAAAGAGA  
M S H H V P P M E D C K E Q E P I M D N N I S L  
GGTGCCTTTTGAGAGACCTGCTGTCATAGAGAAGCTCACGGCAAATATGGGAAAGCGCAAAAGCTCCACT 840  
CCACGGAAACTCTCTGGACGACAGTATCTCTCGAGTGCCGTTTATACCCTTTGCGTTTTTCGAGGTGA  
V P F E R P A V I E K L T A N M G K R K S S T  
CCTCAGAAGTTTGTGGGGGAAAAGCTTATGCGATTGAGCTACCCAGATATTCATTTTGATATGAACTTAA 910  
GGAGTCTTCAAACACCCCTTTTGAATACGCTAAGTCGATGGGTCTATAAGTAAACTATACTTGAATT  
P Q K F V G E K L M R F S Y P D I H F D M N L  
CATATGAGAAGGAGGCTGAGCTGATGCAGTCTCATATGATGGACCAAGCCATCAACAATGCAATCACCTA 980  
GTATACTCTTCTCCGACTCGACTACGTCAGAGTATACTACCTGGTTCGGTAGTTGTTACGTTAGTGGAT  
T Y E K E A E L M Q S H M M D Q A I N N A I T Y  
CCTTGGAGCTGAGGCCCTTACCCTCTGATGCAGCATGCACCAAGCACAATCGCTGAGGTGGCCCCAGTT 1050  
GGAACCTCGACTCCGGGAAGTGGGAGACTACGTCGTACGTGGTTTCGTGTTAGCGACTCCACCGGGGTCAA  
L G A E A L H P L M Q H A P S T I A E V A P V  
ATAAGCTCAGCTTATTCTCAGGTCTATCATCAAACAGGATAGAAAGACCCATTAGCAGGGAAACATCTG 1120  
TATTCGAGTCGAATAAGAGTCCAGATAGTAGGTTTGTCTATCTTTCTGGGTAATCGTCCCTTTGTAGAC  
I S S A Y S Q V Y H P N R I E R P I S R E T S  
ATAGTCACGAAAACAACATGGATGGCCCCATCTCTCTCATCAGACCAAAGAGTCGACCCCAGGAAAGAGA 1190  
TATCAGTGCTTTTGTGTACCTACCGGGGTAGAGAGAGTAGTCTGGTTTCTCAGCTGGGGTCCTTTCTCT  
D S H E N N M D G P I S L I R P K S R P Q E R E  
GGCCTCGCCCAGCAATAGCTGCCTCGATTCTACTGACTCAGAAAGTAGCCATGATGACCGCCAGTCCTAC 1260  
CCGGAGCGGGTCGTTATCGACGGAGCTAAGATGACTGAGTCTTTCATCGGTACTACTGGCGGTGAGGATG  
A S P S N S C L D S T D S E S S H D D R Q S Y

FIG. 3

CAAGGAAACCCTGCCTTAAATCCCAAGAGGAAACAAAGCCCAGCTTACATGAAGGAGGATGTCAAGGCTT 1330  
 GTTCCTTTGGGACGGAATTTAGGGTTCTCCTTTGTTTCGGGTGCAATGTACTTCCTCCTACAGTTCCGAA  
 Q G N P A L N P K R K Q S P A Y M K E D V K A  
 TGGATGCTACCAAGGCCCCCAAGGGCTCTCTGAAGGACATCTATAAGGTTTTCAATGGAGAAGGAGAACA 1400  
 ACCTACGATGGTTCCGGGGGTTCGAGAGACTTCCTGTAGATATTCCAAAAGTTACCTCTTCCTCTTGT  
 L D A T K A P K G S L K D I Y K V F N G E G E Q  
 GATAAGGGCCTTCAAGTGTGAGCACTGCCGAGTCCTTTTTCTAGACCATGTCATGTACACCATTACATG 1470  
 CTATTCGGAAGTTCACACTCGTGACGGCTCAGGAAAAAGATCTGGTACAGTACATGTGGTAAGTGTAC  
 I R A F K C E H C R V L F L D H V M Y T I H M  
 GGTGCCATGGCTACCGGGACCCACTGGAATGCAACATCTGTGGCTACAGAAGCCAGGACCGCTACGAAT 1540  
 CCAACGGTACCGATGGCCCTGGGTGACCTTACGTTGTAGACACCGATGTCTTCGGTCCTGGCGATGCTTA  
 G C H G Y R D P L E C N I C G Y R S Q D R Y E  
 TTTCATCACACATTGTTGGGGGGCAGCACACATTCCACTAGGCGTTTGCATTCCAAGG 1598  
 AAAGTAGTGTGTAACAACCCCCGTCGTGTGTAAGGTGATCCGCAAACGTAAGGTTCC  
 F S S H I V G G Q H T F H . A F A F Q G

FIG. 3  
 (3 of 3)

ATGGAACAGACGCTATTGATGGCTATATAACATGTGACAATGAGCTTTCACCCGAAGGGGAACACGCCA 70  
 TACCTTTGTCTGCGATAACTACCGATATATTGTACACTGTTACTCGAAAGTGGGCTTCCCTTGTGCGGT  
 M E T D A I D G Y I T C D N E L S P E G E H A  
 ATATGGCCATTGACCTCACCTCAAGCACGCCCAATGGACAGCACGCCCTCGCCAAGTCACATGACAAGCAC 140  
 TATACCGGTAAGTGGAGTGGAGTTCGTGCGGGTTACCTGTCTGTGCGGAGCGGTTCAAGTGTACTGTTCTGT  
 N M A I D L T S S T P N G Q H A S P S H M T S T  
 AAATTCTGTAAAGCTGGAAATGCAGAGTGATGAAGAGTGTGACAGGCAGCCCCGAGCCGTGAGGATGAG 210  
 TTTAAGACATTTGACCTTTACGTCTCACTACTTCTCACACTGTCCGTGCGGGGACTCGGCACTCCTACTC  
 N S V K L E M Q S D E E C D R Q P L S R E D E  
 ATCAGGGGCCACGATGAGGGGAGCAGCCTAGAAGAACCCTAATTGAGAGCAGCGAGGTGGCCGACAACA 280  
 TAGTCCCCGGTGCTACTCCCTCGTCGGATCTTCTTGGGGATTAAGTCTCGTCGCTCCACCGGCTGTTGT  
 I R G H D E G S S L E E P L I E S S E V A D N  
 GGAAAGTCCAGGACCTTCAAGGCGAGGGAGGAATCCGGCTTCCGAATGGTGAGCGGCCCTTCCACTGTAA 350  
 CCTTTCAGGTCCTGGAAGTTCGGCTCCCTCCTTAGGCCGAAGGCTTACCACTCGCCGGGAAGGTGACATT  
 R K V Q D L Q G E G G I R L P N G E R P F H C N  
 CCAGTGGGAGCTTCTTTTACCCAGAAGGGCAACCTTCTGAGACACATAAAGTTACACTCTGGAGAGAAG 420  
 GGTACGCTCGAAGAAAATGGGTCTTCCCGTTGGAAGACTCTGTGTATTTCATGTGAGACCTCTCTTC  
 Q C G A S F T Q K G N L L R H I K L H S G E K  
 CCCTTCAAATGTCCTTCTGTAGCTATGCTTGTAGAAGAAGGGACGCTCTCACAGGACACCTCAGGACCC 490  
 GGGAAAGTTTACAGGAAAGACATCGATACGAACATCTTCTTCCCTGCGAGAGTGTCTGTGGAGTCTTGGG  
 P F K C P F C S Y A C R R R D A L T G H L R T  
 ATTCTGTGGGTAAACCTCACAAGTGTAAGTGTGAGGCGAAGCTACAAGCAGCGCACGTCACTGGAGGA 560  
 TAAGACACCCATTTGGAGTGTTCACATTGATGACACCGGCTTCGATGTTCTGTCGCGTGCAGTGACCTCCT  
 H S V G K P H K C N Y C G R S Y K Q R T S L E E  
 ACACAAGGAACGCTGTCACAAGTATCTCCAGAATGTCAGCATGGAGGCTGCCGGGCAGGTCATGAGTCAC 630  
 TGTGTTCTTGGACAGTGTGATAGAGGTCTTACAGTCGTACCTCCGACGGCCCGTCCAGTACTCAGTG  
 H K E R C H N Y L Q N V S M E A A G Q V M S H

FIG. 4  
 (1 of 3)

CATGTACCGCCTATGGAAGATTGTAAGGAACAAGAGCCTATCATGGACAACAATATTTCTCTGGTGCCTT 700  
 GTACATGGCGGATACCTTCTAACATTCCTTGTTCTCGGATAGTACCTGTTGTTATAAAGAGACCACGGAA  
 H V P P M E D C K E Q E P I M D N N I S L V P  
 TTGAGAGACCTGCTGTCATAGAGAAGCTCACGGCAAATATGGGAAAGCGCAAAAGCTCCACTCCTCAGAA 770  
 AACTCTCTGGACGACAGTATCTCTTCGAGTGCCGTTTATACCCTTTCGCGTTTTTCGAGGTGAGGAGTCTT  
 F E R P A V I E K L T A N M G K R K S S T P Q K  
 GTTTGTGGGGGAAAAGCTTATGCGATTGAGCTACCCAGATATTCATTTTGATATGAACTTAACATATGAG 840  
 CAAACACCCCCTTTTCGAATACGCTAAGTCGATGGGTCTATAAGTAAACTATACTTGAATTGTATACTC  
 F V G E K L M R F S Y P D I H F D M N L T Y E  
 AAGGAGGCTGAGCTGATGCAGTCTCATATGATGGACCAAGCCATCAACAATGCAATCACCTACCTTGGAG 910  
 TTCCTCCGACTCGACTACGTCAGAGTATACTACCTGGTTCGGTAGTTGTTACGTTAGTGGATGGAACCTC  
 K E A E L M Q S H M M D Q A I N N A I T Y L G  
 CTGAGGCCCTTCACCCTCTGATGCAGCATGCACCAAGCACAATCGCTGAGGTGGCCCCAGTTATAAGCTC 980  
 GACTCCGGGAAGTGGGAGACTACGTCGTACGTGGTTCGTGTTAGCGACTCCACCGGGGTCAATATTCGAG  
 A E A L H P L M Q H A P S T I A E V A P V I S S  
 AGCTTATTCTCAGGTCTATCATCCAAACAGGATAGAAAGACCCATTAGCAGGGAAACATCTGATAGTCAC 1050  
 TCGAATAAGAGTCCAGATAGTAGGTTTGTCTATCTTTCTGGGTAATCGTCCCTTTGTAGACTATCAGTG  
 A Y S Q V Y H P N R I E R P I S R E T S D S H  
 GAAAACAACATGGATGGCCCCATCTCTCTCATCAGACCAAGAGTCGACCCAGGAAAGAGAGGCCTCGC 1120  
 CTTTGTGTGACCTACCGGGGTAGAGAGAGTAGTCTGGTTTCTCAGCTGGGGTCCTTTCTCTCCGGAGCG  
 E N N M D G P I S L I R P K S R P Q E R E A S  
 CCAGCAATAGCTGCCTCGATTCTACTGACTCAGAAAGTAGCCATGATGACCGCCAGTCCTACCAAGGAAA 1190  
 GGTCGTTATCGACGGAGCTAAGATGACTGAGTCTTTCATCGGTACTACTGGCGGTCAGGATGGTTCCTTT  
 P S N S C L D S T D S E S S H D D R Q S Y Q G N  
 CCCTGCCTTAAATCCCAAGAGGAAACAAAGCCCAGCTTACATGAAGGAGGATGTCAAGGCTTTGGATGCT 1260  
 GGGACGGAATTTAGGGTTCTCCTTTGTTTCGGGTGCAATGTACTTCCTCCTACAGTYCCGAAACCTACGA  
 P A L N P K R K Q S P A Y M K E D V K A L D A

FIG. 4

ACCAAGGCCCCCAAGGGCTCTCTGAAGGACATCTATAAGGTTTTCAATGGAGAAGGAGAACAGATAAGGG 1330  
 TGGTTCCGGGGGTTCCCGAGAGACTTCCTGTAGATATTCCAAAAGTTACCTCTTCCTCTTGTCTATTCCC  
 T K A P K G S L K D I Y K V F N G E G E Q I R  
 CCTTCAAGTGTGAGCACTGCCGAGTCCTTTTTCTAGACCATGTCATGTACACCATTACATGGGTTGCCA 1400  
 GGAAGTTCACACTCGTGACGGCTCAGGAAAAAGATCTGGTACAGTACATGTGGTAAGTGTACCCAACGGT  
 A F K C E H C R V L F L D H V M Y T I H M G C H  
 TGGCTACCGGGACCCACTGGAATGCAACATCTGTGGCTACAGAAGCCAGGACCGCTACGAATTTTCATCA 1470  
 ACCGATGGCCCTGGGTGACCTTACGTTGTAGACACCGATGTCTTCGGTCCTGGCGATGCTTAAAAGTAGT  
 G Y R D P L E C N I C G Y R S Q D R Y E F S S  
 CACATTGTTGGGGGGCAGCACACATTCCACTAGGCGTTTGCATTCCAAGG 1520  
 GTGTAACAACCCCCCGTCGTGTGTAAGGTGATCCGCAACGTAAGGTTCC  
 H I V G G Q H T F H . A F A F Q G

FIG. 4  
 (3 of 3)



1/1 31/11  
GCC CGG GCA GGT CGC ATT GCT ATA GCA CTG ACT GAC CTC TCT CTC TCT CTT TTT TTT CCT  
A R A G R I A I A L T D L S L S L F F P  
61/21 91/31  
CTT TCC TGA AAC CCG ACA TTG TCA CCT CCT CTT TGA GGG TTA GAA GAA GCT GAG ATC TCC  
L S \* N P T L S P P L \* G L E E A E I S  
121/41 151/51  
CGA CAG AGC TGG AAA TGG TGA TGA ATC TTT TTT AAT CAA AGG ACA ATT TCT TTT CAT TGC  
R Q S W K W \* \* I F F N Q R T I S F H C  
181/61 211/71  
ACT TTG ACT ATG GAA ACA GAG GCT ATT GAT GGC TAT ATA ACG TGT GAC AAT GAG CTT TCA  
T L T M E T E A I D G Y I T C D N E L S  
241/81 271/91  
CCC GAA AGG GAG CAC TCC AAT ATG GCA ATT GAC CTC ACC TCA AGC ACA CCC AAT GGA CAG  
P E R E H S N M A I D L T S S T P N G Q  
301/101 331/111  
CAT GCC TCA CCA AGT CAC ATG ACA AGC ACA GAT TCA GTA AAG CTA GAA ATG CAG AGT GAT  
H A S P S H M T S T D S V K L E M Q S D  
361/121 391/131  
GAA GAG TGT GAC AGG AAA CCC CTG AGC CGT GAA GAT GAG ATC AGG GGC CAT GAT GAG GGT  
E E C D R K P L S R E D E I R G H D E G  
421/141 451/151  
AGC AGC CTA GAA GAA CCC CTA ATT GAG AGC AGC GAG GTG GCT GAC AAC AGG GAA GTC CAG  
S S L E E P L I E S S E V A D N R E V Q  
481/161 511/171  
GAG CTT CAA GGC GAG GGA GGA ATC CGG CTT CCG AAT GGT AAA CTG AAA TGT GAC GTC TGT  
L Q G E G G I R L P N G K L K C D V C  
541/181 571/191  
GGC ATG GTT TGC ATT GGG CCC AAT GTG CTT ATG GTA CAT AAA AGG AGT CAC ACT GGT GAA  
M V C I G P N V L M V H K R S H T G E  
601/201 631/211  
CGC CCC TTC CAC TGT AAC CAG TGT GGA GCT TCT TTT ACT CAG AAG GGC AAC CTT CTG AGA  
R P F H C N Q C G A S F T Q K G N L L R  
661/221 691/231  
CAC ATA AAG TTA CAC TCT GGA GAG AAG CCG TTC AAA TGT CCT TTC TGT AGT CAC GCC TGT  
H I K L H S G E K P F K C P F C S H A C  
721/241 751/251  
AGA AGA AGG GAC GCC CTC ACA GGA TAC CTC AGG ACC CAT TCT GTG GGT AAA CCT CAC AAG  
R R D A L T G Y L R T H S V G K P H K  
781/261 811/271  
TGC AAC TAC TGT GGA CGA AGC TAC AAG CAG CGC AGT TCA CTG GAG GAG CAC AAG GAA CGC  
C N Y C G R S Y K Q R S S L E E H K E R  
841/281 871/291  
TGC CAC AAC TAT CTC CAG AAT GTC AGC ATG GAG GCT GCT GGG CAG GTC ATG AGT CAC CAT  
C H N Y L Q N V S M E A A G Q V M S H H  
901/301 931/311  
GTA CCT CCT ATG GAA GAT TGT AAG GAA CAA GAG CCT ATT ATG GAC AAC AAT ATT TCT CTG  
V P P M E D C K E Q E P I M D N N I S L  
961/321 991/331  
GTG CCT TTT GAG AGA CCT GCT GTC ATA GAG AAG CTC ACG GGG AAT ATG GGA AAA CGT AAA  
V P F E R P A V I E K L T G N M G K R K  
1021/341 1051/351  
AGC TCC ACT CCA CAA AAG TTT GTG GGG GAA AAG CTC ATG CGA TTC AGC TAC CCA GAT ATT  
S S T P Q K F V G E K L M R F S Y P D I  
1081/361 1111/371  
CAC TTT GAT ATG AAC TTA ACA TAT GAG AAG GAG GCT GAG CTG ATG CAG TCT CAT ATG ATG  
H F D M N L T Y E K E A E L M Q S H M M  
1141/381 1171/391  
GAC CAA GCC ATC AAC AAT GCA ATC ACC TAC CTT GGA GCT GAG GCC CTT CAC CCT CTG ATG  
D Q A I N N A I T Y L G A E A L H P L M  
1201/401 1231/411  
CAG CAC CCG CCA AGC ACA ATC GCT GAA GTG GCC CCA GTT ATA AGC TCA GCT TAT TCT CAG  
Q H P P S T I A E V A P V I S S A Y S Q

FIG. 5  
(1 of 2)

1261/421  
 GTC TAT CAT CCA AAT AGG ATA GAA AGA CCC ATT AGC AGG GAA ACT GCT GAT AGT CAT GAA  
 V Y H P N R I E R P I S R E T A D S H E  
 1321/441  
 AAC AAC ATG GAT GGC CCC ATC TCT CTC ATC AGA CCA AAG AGT CGA CCC CAG GAA AGA GAG  
 N N M D G P I S L I R P K S R P Q E R E  
 1381/461  
 GCC TCT CCC AGC AAT AGC TGC CTG GAT TCC ACT GAC TCA GAA AGC AGC CAT GAT GAC CAC  
 A S P S N S C L D S T D S E S S H D D H  
 1441/481  
 CAG TCC TAC CAA GGA CAC CCT GCC TTA AAT CCC AAG AGG AAA CAA AGC CCA GCT TAC ATG  
 Q S Y Q G H P A L N P K R K Q S P A Y M  
 1501/501  
 AAG GAG GAT GTC AAA GCT TTG GAT ACT ACC AAG GCT CCT AAG GGC TCT CTG AAG GAC ATC  
 K E D V K A L D T T K A P K G S L K D I  
 1561/521  
 TAC AAG GTC TTC AAT GGG GAA GGA GAA CAG ATT AGG GCC TTC AAG TGT GAG CAC TGC CGA  
 Y K V F N G E G E Q I R A F K C E H C R  
 1621/541  
 GTC CTT TTC CTA GAC CAT GTC ATG TAC ACC ATT CAC ATG GGT TGC CAT GGC TAC CGG GAC  
 V L F L D H V M Y T I H M G C H G Y R D  
 1681/561  
 CCA CTG GAA TGT AAC ATC TGT GGC TAC AGA AGC CAG GAC CGT TAT GAG TTT TCA TCA CAC  
 P L E C N I C G Y R S Q D R Y E F S S H  
 1741/581  
 ATT GTT CGA GGG GAG CAC ACA TTC CAC TAG GCC TTT TCA TTC CAA AGG GGA CCC TAT GAA  
 I V R G E H T F H \* A F S F Q R G P Y E  
 1801/601  
 GTA AAG ACT GCA CAT GAA GAA ATA CTG CAC TTA CAA TCC CAC CTT TCC TCA AAT GTT GTA  
 V K T A H E E I L H L Q S H L S S N V V  
 1861/621  
 CCT TTT ATT TTT TTA ATA TAA TAC TGG TGA TAA TCT TAT TTT GTG GAG CAG TGT CAT TTG  
 P F I F L I \* Y W \* \* S Y F V E Q C H L  
 1921/641  
 CTC TGC T  
 C

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1  ATGGAACAGACGCTATTGATGGCTATATAACATGTGACAATGAGCTTTC 50
   |||||||
190 ATGGAACAGAGGCTATTGATGGCTATATAACGTGTGACAATGAGCTTTC 239
   |||||||
51  ACCCGAAGGGGAACACGCCAATATGGCCATTGACCTCACCTCAAGCACGC 100
   |||||||
240 ACCCGAAGGGGAGCACTCCAATATGGCAATTGACCTCACCTCAAGCACAC 289
   |||||||
101 CCAATGGACAGCAGCCTCGCCAAGTCACATGACAAGCAGAAATTCTGTA 150
   |||||||
290 CCAATGGACAGCATGCCTCACCAAGTCACATGACAAGCAGATTTCAGTA 339
   |||||||
151 AAGCTGGAAATGCAGAGTGATGAAGAGTGTGACAGGCAGCCCTGAGCCG 200
   |||||||
340 AAGCTAGAAATGCAGAGTGATGAAGAGTGTGACAGGAAACCCCTGAGCCG 389
   |||||||
201 TGAGGATGAGATCAGGGGCCACGATGAGGGGAGCAGCCTAGAAGAACCCC 250
   |||||||
390 TGAAGATGAGATCAGGGGCCATGATGAGGGTAGCAGCCTAGAAGAACCCC 439
   |||||||
251 TAATTGAGAGCAGCGAGGTGGCCGACAACAGGAAAGTCCAGGACCTTCAA 300
   |||||||
440 TAATTGAGAGCAGCGAGGTGGCTGACAACAGGGAAGTCCAGGAGCTTCAA 489
   |||||||
301 GGCGAGGGAGGAATCCGGCTTCCGAATGGTAAACTGAAATGTGACGTCTG 350
   |||||||
490 GGCGAGGGAGGAATCCGGCTTCCGAATGGTAAACTGAAATGTGACGTCTG 539
   |||||||
351 TGGCATGGTTTGCATTGGGCCCAATGTGCTTATGGTACATAAAAGGAGTC 400
   |||||||
540 TGGCATGGTTTGCATTGGGCCCAATGTGCTTATGGTACATAAAAGGAGTC 589
   |||||||
401 ACACTGGTGAGCGGCCCTTCCACTGTAACCAAGTGGGAGCTTCTTTTACC 450
   |||||||
590 ACACTGGTGAACGCCCTTCCACTGTAACCAAGTGTGGAGCTTCTTTTACT 639
   |||||||
451 CAGAAGGGCAACCTTCTGAGACACATAAAGTTACACTCTGGAGAGAAGCC 500
   |||||||
640 CAGAAGGGCAACCTTCTGAGACACATAAAGTTACACTCTGGAGAGAAGCC 689
   |||||||
501 CTTCAAATGTCCTTTCTGTAGCTATGCTTGTAGAAGAAGGGACGCTCTCA 550
   |||||||
690 GTTCAAATGTCCTTTCTGTAGTCACGCCTGTAGAAGAAGGGACGCCCTCA 739
   |||||||
551 CAGGACACCTCAGGACCCATTCTGTGGGTAAACCTCACAAGTGTAAGTAC 600
   |||||||
740 CAGGATACCTCAGGACCCATTCTGTGGGTAAACCTCACAAGTGCAACTAC 789
   |||||||
601 TGTGGCCGAAGCTACAAGCAGCGCAGTCACTGGAGGAACACAAGGAACG 650
   |||||||
790 TGTGGACGAAGCTACAAGCAGCGCAGTCACTGGAGGAGCACAAGGAACG 839
   |||||||
651 CTGTCACAACTATCTCCAGAATGTCAGCATGGAGGCTGCCGGGCAGGTCA 700
   |||||||
840 CTGCCACAACTATCTCCAGAATGTCAGCATGGAGGCTGCTGGGCAGGTCA 889
   |||||||
701 TGAGTCACCATGTACCGCCTATGGAAGATTGTAAGGAACAAGAGCCTATC 750
   |||||||
890 TGAGTCACCATGTACCTCCTATGGAAGATTGTAAGGAACAAGAGCCTATT 939
   |||||||
751 ATGGACAACAATATTTCTCTGGTGCCTTTTGAGAGACCTGCTGTCATAGA 800
   |||||||

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FIG. 6  
(1 of 3)

940 ATGGACAACAATATTTCTCTGGTGCCTTTTGAGAGACCTGCTGTCATAGA 989  
 801 GAAGCTCACGGCAAATATGGGAAAGCGCAAAGCTCCACTCCTCAGAAGT 850  
 |||||  
 990 GAAGCTCACGGGGAATATGGGAAAACGTAAAAGCTCCACTCCACAAAAGT 1039  
 851 TTGTGGGGGAAAAGCTTATGCGATTACCTACCCAGATATTCATTTTGAT 900  
 |||||  
 1040 TTGTGGGGGAAAAGCTCATGCGATTACCTACCCAGATATTCACTTTGAT 1089  
 901 ATGAACTTAACATATGAGAAGGAGGCTGAGCTGATGCAGTCTCATATGAT 950  
 |||||  
 1090 ATGAACTTAACATATGAGAAGGAGGCTGAGCTGATGCAGTCTCATATGAT 1139  
 951 GGACCAAGCCATCAACAATGCAATCACCTACCTTGGAGCTGAGGCCCTTC 1000  
 1140 GGACCAAGCCATCAACAATGCAATCACCTACCTTGGAGCTGAGGCCCTTC 1189  
 1001 ACCCTCTGATGCAGCATGCACCAAGCACAATCGCTGAGGTGGCCCCAGTT 1050  
 |||||  
 1190 ACCCTCTGATGCAGCACCCGCCAAGCACAATCGCTGAAGTGGCCCCAGTT 1239  
 1051 ATAAGCTCAGCTTATTCTCAGGTCTATCATCCAACAGGATAGAAAGACC 1100  
 |||||  
 1240 ATAAGCTCAGCTTATTCTCAGGTCTATCATCCAATAGGATAGAAAGACC 1289  
 1101 CATTAGCAGGGAAACATCTGATAGTCACGAAAACAACATGGATGGCCCCA 1150  
 |||||  
 1290 CATTAGCAGGGAAACTGCTGATAGTCATGAAAACAACATGGATGGCCCCA 1339  
 1151 TCTCTCTCATCAGACCAAAGAGTCGACCCCAGGAAAGAGAGGCCTCGCCC 1200  
 |||||  
 1340 TCTCTCTCATCAGACCAAAGAGTCGACCCCAGGAAAGAGAGGCCTCTCCC 1389  
 1201 AGCAATAGCTGCCTCGATTCTACTGACTCAGAAAGTAGCCATGATGACCG 1250  
 |||||  
 1390 AGCAATAGCTGCCTGGATTCCACTGACTCAGAAAGCAGCCATGATGACCA 1439  
 1251 CCAGTCCTACCAAGGAAACCCTGCCTTAAATCCCAAGAGGAAACAAAGCC 1300  
 |||||  
 1440 CCAGTCCTACCAAGGACACCCTGCCTTAAATCCCAAGAGGAAACAAAGCC 1489  
 1301 CAGCTTACATGAAGGAGGATGTCAAGGCTTTGGATGCTACCAAGGCCCCC 1350  
 |||||  
 1490 CAGCTTACATGAAGGAGGATGTCAAAGCTTTGGATACTACCAAGGCTCCT 1539  
 1351 AAGGGCTCTCTGAAGGACATCTATAAGGTTTTCAATGGAGAAGGAGAACA 1400  
 |||||  
 1540 AAGGGCTCTCTGAAGGACATCTACAAGGCTTCAATGGGGAAGGAGAACA 1589  
 1401 GATAAGGGCCTTCAAGTGTGAGCACTGCCGAGTCCTTTTTCTAGACCATG 1450  
 |||||  
 1590 GATTAGGGCCTTCAAGTGTGAGCACTGCCGAGTCCTTTTTCTAGACCATG 1639  
 1451 TCATGTACACCATTACATGGGTTGCCATGGCTACCGGGACCCACTGGAA 1500  
 |||||  
 1640 TCATGTACACCATTACATGGGTTGCCATGGCTACCGGGACCCACTGGAA 1689  
 1501 TGCAACATCTGTGGCTACAGAAGCCAGGACCGCTACGAATTTTCATCACA 1550  
 |||||  
 1690 TGTAACATCTGTGGCTACAGAAGCCAGGACCGTTATGAGTTTTTCATCACA 1739

FIG. 6  
 (2 of 3)



1	METEAI	DGYIT	CDNEL	S	PEREHS	NMAID	LTSST	PNGQ	HASPS	HMTSTD	SV	50
1	METEAI	DGYIT	CDNEL	S	PEREHS	NMAID	LTSST	PNGQ	HASPS	HMTSTD	SV	50
51	KLEM	QSD	E	E	C	D	R	K	P	L	S	100
51	KLEM	QSD	E	E	C	D	R	K	P	L	S	100
101	GEGGI	R	L	P	N	G	K	L	C	D	V	150
101	GEGGI	R	L	P	N	G	K	L	C	D	V	150
151	QKGN	L	L	R	H	I	K	L	H	S	G	200
151	QKGN	L	L	R	H	I	K	L	H	S	G	200
201	CGRS	Y	Q	R	S	S	L	E	E	H	K	250
201	CGRS	Y	Q	R	S	S	L	E	E	H	K	250
251	MDNN	I	S	L	V	P	F	F	E	R	P	300
251	MDNN	I	S	L	V	P	F	F	E	R	P	300
301	MNLT	Y	E	K	E	A	E	L	M	Q	S	350
301	MNLT	Y	E	K	E	A	E	L	M	Q	S	350
351	ISSA	Y	S	Q	V	Y	H	P	N	R	I	400
351	ISSA	Y	S	Q	V	Y	H	P	N	R	I	400
401	SNSC	L	D	S	T	D	S	E	S	S	H	450
401	SNSC	L	D	S	T	D	S	E	S	S	H	450
451	KGSL	K	D	I	Y	K	V	F	N	G	E	500
451	KGSL	K	D	I	Y	K	V	F	N	G	E	500
501	CNIC	G	Y	R	S	Q	D	R	Y	E	F	526
501	CNIC	G	Y	R	S	Q	D	R	Y	E	F	526

FIG. 7